

GenCore version 5.1.4_p5_4578
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OM nucleic - nucleic search, using sw model

Run on: May 8, 2003, 14:51:24 ; Search time 6124 Seconds
(without alignments)
13439.821 Million cell updates/sec

Title: US-09-497-822C-18

Perfect score: 5082

Sequence: 1 gagctctgacaaaattgag.....acaagcaacaaaaaaa 5082

Scoring table: IDENTITY NUC

Gapop 10.0 , Gapext 1.0

Searched: 16154066 seqs, 8097743376 residues

Total number of hits satisfying chosen parameters: 32308132

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

```

1: em_estba:*
2: em_esthum:*
3: em_estin:*
4: em_estmu:*
5: em_estov:*
6: em_estpl:*
7: em_estro:*
8: em_hic:*
9: gb_estl:*
10: gb_est2:*
11: gb_hic:*
12: gb_est3:*
13: gb_est4:*
14: gb_est5:*
15: em_estfun:*
16: em_estcom:*
17: gb_gss:*
18: em_gss_hum:*
19: em_gss_inv:*
20: em_gss_pln:*
21: em_gss_vrt:*
22: em_gss_fun:*
23: em_gss_mam:*
24: em_gss_mus:*
25: em_gss_other:*
26: em_gss_pro:*
27: em_gss_rtd:*

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	571.8	11.3	654	10 AW951855	AW951855 EST363925
2	529	10.4	532	9 AL704463	AL704463 DKFZp886A
3	519.4	10.2	634	10 BB612466	BB612466 BB612466
4	501.4	9.9	568	9 AA524966	AA524966 nh35c11.s
5	462.2	9.1	724	9 AI317423	AI317423 uj22e09.y
6	380.6	7.5	388	9 AA229063	AA229063 nc49g07.5

c	7	369	7.3	369	9	AA229062	AA229062 nc49g07.5
	8	368.4	7.2	628	10	BB617970	BB617970 BB617970
	9	361	7.1	413	14	T28396	T28396 EST41738 Hu
	10	358.4	7.1	573	10	AW619116	AW619116 436 MARC
	11	357.8	7.0	637	9	AI785019	AI785019 uj22e09.x
	12	347.4	6.8	349	9	AA230070	AA230070 nc49b06.s
	13	346	6.8	379	9	AA659567	AA659567 nt63a03.s
	14	319	6.3	536	9	AI315085	AI315085 uj23g04.k
	15	293.2	5.8	498	17	AZ017963	AZ017963 RPCI-23-2
	16	285.4	5.6	292	9	AA229714	AA229714 nc49b06.f
	17	247.6	4.9	395	17	AZ267276	AZ267276 RPCI-23-1
	18	246.4	4.8	673	13	BI887100	BI887100 ZF637-1-0
	19	238	4.7	247	9	AI659563	AI659563 tui2d12.x
	20	234.2	4.6	396	10	AW619096	AW619096 424 MARC
	21	226.8	4.5	557	13	BI979490	BI979490 ft88b09.y
	22	221.4	4.4	664	9	AL709143	AL709143 DKFZp886L
	23	216.8	4.3	667	13	BI183393	BI183393 UNL-P-FN-
	24	214.6	4.2	413	9	AI326670	AI326670 mo60g04.y
	25	203.4	4.0	378	9	AI893550	AI893550 mo60g04.x
	26	196.2	3.9	322	9	AI317523	AI317523 uj23g04.y
	27	193.8	3.8	1033	14	BQ049864	BQ049864 AGENCOURT
	28	193.2	3.8	339	10	AW619117	AW619117 437 MARC
	29	190.6	3.8	389	9	AA089319	AA089319 mo60g04.y
	30	184.6	3.6	798	9	AU136010	AU136010 AU136010
	31	178.8	3.5	582	14	BM714196	BM714196 UI-E-EJO-
	32	178.4	3.5	647	14	BM714773	BM714773 UI-E-EJO-
	33	174.6	3.4	613	13	BG938686	BG938686 cn27g02.x
	34	173	3.4	643	12	BG345621	BG345621 dg89g10.y
	35	171.8	3.4	621	12	BG866115	BG866115 dad73b08
	36	171.6	3.4	627	12	BG817008	BG817008 dad68h09
	37	167.8	3.3	441	10	BB850026	BB850026 BB850026
	38	167.6	3.3	293	9	AA561201	AA561201 vl28g06.f
	39	164.6	3.2	546	13	BG97346	BG97346 MR4-HT105
	40	163.8	3.2	667	10	BB666485	BB666485 BB666485
	41	163.6	3.2	720	9	AU139958	AU139958 AU139958
	42	162.2	3.2	831	12	BG614664	BG614664 602642157
	43	159.4	3.1	521	10	AW910225	AW910225 ur79c10.y
	44	158.4	3.1	464	17	AZ303301	AZ303301 UP_479-13
	45	157.6	3.1	459	9	AA252234	AA252234 zr63h08.f

ALIGNMENTS

RESULT 1
AW951855
LOCUS
DEFINITION
ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM
REFERENCE
AUTHORS
TITLE
JOURNAL
COMMENT
FEATURES
source

AW951855
EST363925
AW951855
AW951855.1
EST.
human.
Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 654)
Hegde, P., Qi, R., Abernathy, K., Dharap, S., Gaspard, R., Gay, C., Holt, J.E., Saeed, A.I., Sharov, V., Lee, N.H., Yeatman, T.J. and Quackenbush, J.
Assessment of gene expression patterns in a model of colon tumor metastasis using a 19,200 element cDNA microarray
Unpublished (2000)
Contact: John Quackenbush
The Institute for Genomic Research
9712 Medical Center Dr., Rockville, MD 20850, USA
Tel: 301 838 3528
Fax: 301 838 0208
Email: johnqu@tigr.org
Plate: 32
Seq primer: Reverse.
Location/Qualifiers
1..654
/organism="Homo sapiens"

[illegible]

mouse mouse.
Mus musculus
Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
1 (bases 1 to 724)
Marra.M., Hallier.L., Allen.M., Bowles.M., Dietrich.N., Dubuque.T.,
Geisel.S., Kucaba.T., Lacy.M., Le.M., Martin.J., Morris.M.,
Schellenberg.K., Steptoe.M., Tan.F., Underwood.K., Moore.B.,
Theising.B., Wylie.T., Lennon.G., Soares.B., Willson.R. and
Waterston.R.
The WashU-HMMI Mouse EST Project
Unpublished (1996)
Contact: Marra M/Mouse EST Project
WashU-HMMI Mouse EST Project
Washington University School of MedicineP
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
Tel: 314 286 1800
Fax: 314 286 1810
Email: mouseest@watson.wustl.edu
This clone is available royalty-free through LNL; contact the
IMAGE Consortium (info@image.llnl.gov) for further information.
MG1:977004
Sequencing: custom primer used

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Seq primer: custom primer
High quality sequence stop: 515.
Location/Qualifiers
1. 724
/organism="Mus musculus"
/strain="C57BL"
/db_xref="taxon:10090"
/clone="IMAGE:I920713"
/clone_lib="Sugano mouse kidney mkia"
/sex="female"
/dev_stage="adult"
/lab_host="DH10B"
/note="Organ: kidney; Vector: pME18S-FL3; Site_1: DraIII
(CACATGTGTG); Site_2: DraIII (CACCATGTG); 1st strand cDNA
was primed with an oligo(dT) primer
[ATGTGGCCTTTTCTTTTCTTTT]; double-stranded cDNA was
ligated to a DraIII adaptor [TCTGGCCTACTGG], digested
and cloned into distinct DraIII sites of the pME18S-FL3
vector (5' site CACTGTGGT, 3' site CACATGTG). XhoI should
be used to isolate the cDNA insert. Size selection was
performed to exclude fragments <1.5kb. Library
constructed by Dr. Sumio Sugano (University of Tokyo
Institute of Medical Science). Custom primers for
sequencing: 5' end primer CTCTGCTCTAAAGCTGCG and 3' end
primer CGACCTGCAGCTCGAGCAC."
190 a 181 c 192 g 161 t
BASE COUNT
ORIGIN
Query Match 9.1%; Score 462.2; DB 9; Length 724;
Best Local Similarity 82.8%; Pred. No. 3.6e-56;
Matches 564; Conservative 0; Mismatches 113; Indels 4; Gaps 3

```


REFERENCE	1 (bases 1 to 369)	RESULT 8
AUTHORS	NCI-CCAP http://www.ncbi.nlm.nih.gov/ncicgap .	BB617970
TITLE	National Cancer Institute, Cancer Genome Anatomy Project (CGAP), Tumor Gene Index	LOCUS
JOURNAL	Unpublished (1997)	DEFINITION
COMMENT	Contact: Robert Strausberg, Ph.D. Email: cgaps@email.nih.gov Tissue Procurement: W. Marston Linehan, M.D., Rodrigo Chuaqui, M.D., Michael Emmert-Buck, M.D., Ph.D. CDNA Library Preparation: David B. Krizman, Ph.D. DNA Sequencing by: Genome Systems Inc., Greg Lennon, Ph.D. Clone distribution: NCI-CCAP clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at: www-bio.llnl.gov/dbp/image/image.html Seq primer: -28m13 rev1 ET from Amersham High quality sequence stop: 341.	BB617970 RIKEN full-length enriched, adult male pituitary gland Mus musculus cDNA clone 5330428G13 5', mRNA sequence. BB617970 BB617970.1 GI:16457679 EST. house mouse. Mus musculus Eukaryota; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus. 1 (bases 1 to 628) Arakawa,T., Carninci,P., Fukuda,S., Furuno,M., Hanaoka,T., Hara,A., Hiramoto,K., Hori,F., Ishii,Y., Ito,M., Kawai,J., Konno,H., Kouda,M., Koya,S., Matsuyama,T., Miyazaki,A., Nomura,K., Ohno,M., Okazaki,Y., Okido,T., Saito,R., Sakai,C., Sakai,K., Sano,H., Sasaki,D., Shibata,K., Shinagawa,A., Shiraki,T., Sogabe,Y., Suzuki,H., Tagami,M., Tagawa,A., Takahashi,F., Takeda,Y., Tanaka,T., Toya,T., Muramatsu,M. and Hayashizaki,Y. RIKEN Mouse ESTs (Arakawa,T., et al. 2001) Unpublished (2001) Contact: Yoshihide Hayashizaki Laboratory for Genome Exploration Research Group, RIKEN Genomic Sciences Center(GSC), Yokohama Institute The Institute of Physical and Chemical Research (RIKEN) 1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan Tel: 81-45-503-9222 Fax: 81-45-503-9216 Email: genome-res@gsc.riken.go.jp , URL:http://genome.gsc.riken.go.jp/ , Carninci,P., Shibata,Y., Hayatsu,N., Sugahara,Y., Shibata,K., Itoh,M., Konno,H., Okazaki,Y., Muramatsu,M. and Hayashizaki,Y. Normalization and subtraction of cap-trapper-selected cDNAs to prepare full-length cDNA libraries for rapid discovery of new genes. Genome Res. 10 (10), 1617-1630 (2000) wagi,K., Fujiwaki,S., Inoue,K., Togawa,Y., Izawa,M., Ohara,E., Watahiki,M., Yoneda,Y., Ishikawa,T., Ozawa,K., Tanaka,T., Matsuura,S., Kawai,J., Okazaki,Y., Muramatsu,M., Inoue,Y., Kira,A. and Hayashizaki,Y. RIKEN integrated sequence analysis (RISA) system--384-format sequencing pipeline with 384 multicapillary sequencer. Genome Res. 10 (11), 1757-1771 (2000) Konno,H., Fukunishi,Y., Shibata,K., Itoh,M., Carninci,P., Sugahara,Y. and Hayashizaki,Y. Computer-based methods for the mouse full-length cDNA encyclopedia: real-time sequence clustering for construction of a nonredundant cDNA library. Genome Res. 11 (2), 281-289 (2001) Kondo,S., Shinagawa,A., Saito,T., Kiyosawa,H., Yamanaka,I., Aizawa,K., Fukuda,S., Hara,A., Itoh,M., Kawai,J., Shibata,K. and Hayashizaki,Y. Computational Analysis of Full-Length Mouse cDNAs Compared with Human Genome Sequences. Mamm. Genome. 12, 673-677 (2001) Please visit our web site (http://genome.gsc.riken.go.jp) for further details. e mouse tissues.
FEATURES	Location/Qualifiers	FEATURES
SOURCE	1..369	1..628
	/organism="Homo sapiens"	/organism="Mus musculus"
	/db_xref="taxon:9606"	/strain="C57BL/6J"
	/clone="IMAGE:1011516"	/db_xref="taxon:10090"
	/clone_lib="NCI-CCAP_Pr3"	/clone="5330428G13"
	/sex="Male"	/clone_lib="RIKEN full-length enriched, adult male
	/dev_stage="45 years old"	pituitary gland"
	/lab_host="DH10B"	/sex="male"
	/note="Vector: pAMP10; Site_1: NotI; Site_2: EcoRI; 1st strand cDNA was primed with oligo(dT)17 on 50 ng of DNase-treated, total cellular RNA obtained from 5,000-10 fully malignant prostate cancer cells. Double-stranded cDNA was ligated to EcoRI adaptors, 5 cycles of PCR applied to the cDNA with an adaptor-specific primer, and the resulting PCR product subcloned into pAMP10 by the UDG-cloning method (Life Technologies). Average insert size is 600 bp. NOTE: Not directionally cloned. This library was constructed by David Krizman."	/tissue_type="pituitary gland"
	142 a 67 c 93 g 67 t	/dev_stage="adult"
BASE COUNT		/lab_host="DH10B"
ORIGIN		/note="Site_1: Sall; Site_2: BamHI; cDNA library was prepared and sequenced in Mouse Genome Encyclopedia project of Genome Exploration Research Group in Riken Genomic Sciences Center and Genome Science Laboratory in Riken
Query Match	7.3%; Score 369; DB 9; Length 369;	RIKEN. Division of Experimental Animal Research in Riken
Best Local Similarity	100.0%; Pred. No. 7.9e-43;	
Matches 369; Conservative 0; Mismatches 0; Indels 0; Gaps 0;		
QY 4680	CAGATGCTCTTCGCTGTATTAACCTGCACCTACCTCTCTGCAGTGCCTTGGGAATTC 4739	
DB 369	CAGATGCTCTTCGCTGTATTAACCTGCACCTACCTCTCTGCAGTGCCTTGGGAATTC 310	
QY 4740	CTCTATTGATGACAGTCTGTCATGACATGTTCTCGAATCTATTCTGCTGGCTTTT 4799	
DB 309	CTCTATTGATGACAGTCTGTCATGACATGTTCTCGAATCTATTCTGCTGGCTTTT 250	
QY 4800	TTTCTCTTCT 4859	
DB 249	TTTCTCTTCT 190	
QY 4860	TCAGACTTTGCTTCCCATTTGCTGCTTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 4919	
DB 189	TCAGACTTTGCTTCCCATTTGCTGCTTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 130	
QY 4920	AATCTGTGATGATCCCATATGATGCCAGTGTCAAGTTGCTTGTTCAGCAGCTACTCT 4979	
DB 129	AATCTGTGATGATCCCATATGATGCCAGTGTCAAGTTGCTTGTTCAGCAGCTACTCT 70	
QY 4980	GTGCCAGCCACACAAACGTTTACTTATCTATATGCCAGGAAAGTTAGAGAGCTAAGATT 5039	
DB 69	GTGCCAGCCACACAAACGTTTACTTATCTATATGCCAGGAAAGTTAGAGAGCTAAGATT 10	
QY 5040	ATCTGGGGA 5048	
DB 9	ATCTGGGGA 1	

contributed to prepare mouse tissues. 1st strand cDNA was primed with a primer [5', GAGAGAGAGAGATCCAGAGCTTTTTTTTTTTTTTNN 3'], cDNA was prepared by using trehalose thermo-activated reverse transcriptase and subsequently enriched for full-length by cap-trapper. cDNA went through one round of normalization to Rot = 3.0 and subtraction to Rot = 100.0. Second strand cDNA was prepared with the primer adapter of sequence [5', GAGAGAGAGATCTCCAGTAAATTAATATCCCTCCCCCCCC 3']. cDNA was cloned into the XhoI and BamHI sites. Vector: a modified pBluescript KS(+) after bulk excision from Lambda FLC I. Cloning sites, 5' end: SalI; 3' end: BamHI".

209 c	183 g	85 t
-------	-------	------

[illegible]

1804	Y	GAGCAAGAGAGAGGGGAGCGGGTAAAGGAAGTAGTGGAAATTCAGCAGACTCAAGG	1863
3	Db	GAGCAAGAGAGAGAGGAGGAGGATAAGGGAATTCGGTGGAGCTACAGCAGACTCAAGG	62
1864	Y	ATGGAAATGCAATTTAGGGCTTGGGAAGGCTTACCTTCGGCCGCCCTCCAAGACCTACCGA	1923
63	Db	ATGGAGTGTCAATTTAGGGCTTGGGAAGGCTTACCTTCGGCCGCCCTCCAAGACCTACCGA	122
1924	Y	GGAGCTTTCAGAAATCTGTTTCCAGAGCGTGGCGAAGTATCCAGCAACCCGGGCCCCAGG	1983
123	Db	GGAGCTTTCAGAAATCTGTTTCCAGAGCGTGGCGAAGTATCCAGCAACCCGGGCCCCAGG	182
1984	Y	CACCCAGAGCGCGGAGCGGAGCACTCCCGGGCGGAGTTTGTCTGTCTGCAGCAGCAG	2043
183	Db	CACCTTGAGGCGGCTTAACATAGCACCTCCCGGGCGGCTGTTT	223
2044	Y	CAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAG	2103
224	Db	-----ACAGCAGAGG	233
2104	Y	CAGCAAGAGACTAGCCCCAGGAGCAGCAGCAGCAGCAGGAGTGGTTCTTCCCCAA	2163
234	Db	CAGGAGACTAGCCCCGGGGGGGGGCGGAGCAGCAGCAGTGGAGTGGTTCTCTCAA	293
2164	Y	GCCCATCGTAGGGCCCCACAGGCTACCTGTGCTGGATGAGGACAGCAACCTTCACAG	2223
294	Db	GCCACATCAGAGCCCCACAGGCTACCTGTGCTGGAGGAGGAGCAGCAGCTTCACAG	953
2224	Y	CCGAGTCGGCCCTGGAGTGCACCCCGAGAGAGGTTGCTCCAGAGCCTGGAGCGGC	2283
354	Db	CAGCAGCAGCCTCCGAGGGCCACCTGAGAGCAGTGCCTCCCGAGCCTGGGGCGGC	413
2284	Y	GTGGCGCCAGCAAGGGGTCGCCAGCAGCTGCCAGCACTCCGGACGAGGATGACTCA	2343
414	Db	ACGCTCTTGGCAAGGGGTCGCCAGCAGCAGCAGCTCTCCAGATCAGGATGACTCA	473
2344	Y	GTTGCCCATCCACGTTGTCTGCTGGGCCCCACTTTCCCGGCTTAAAGCAGCTGCTCC	2403
474	Db	GCTGCCCATCCACGTTGTCTGCTGGGCCCCACTTTCCAGGCTTAAAGCAGCTGCTCC	533
2404	Y	GCTGACCTTAAAGACATCTTGAGGAGGCGCAGCACCATGCACTCTTCAGCAACGAG	2463
534	Db	GCCGACCTTAAAGACATTTGAACGAGCGCGCACCATGCAACTTTTAGCAGCAGCA	593
2464	Y	CA 2465	
594	Y	CA 595	

RESULT 9	T28396	LOCUS	T28396	413 bp	mRNA	linear	EST 06-SEP-1995
DEFINITION	EST411738	Human uterus Homo sapiens	receptor (HT.1334), mRNA sequence.				CDNA 5' end similar to androgen

ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM

T28396
T28396.1 GI:610494

ORGANISM

REFERENCE AUTHORS

T28396
T28396.1 GI:610494
ESI.
human.
Homo sapiens
Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominoidea; Homo.

Mammalia: Eutheria: Primates: Catarrhini: Hominoidea: Homo.
I (bases 1 to 413)
Adams, M.D., Kerlavage, A.R., Fleischmann, R.D., Fuldner, R.A., Bult,
C.J., Lee, N., Kirkness, E.F., Weinstein, K.G., Gocayne, J.D., White
O., Sutton, G., Blake, J.A., Brandon, R.C., Chiu, M.-W., Clayton, R.A.,
Cline, R.T., Cotton, M.D., Earle-Hughes, J., Fine, L.D., Fitzgerald,
L.M., FitzHugh, W.M., Fritchman, J.L., Geoghagen, N.S.M., Glodex, A.,
Gnehm, C.L., Hanna, M.C., Hedblom, E., Hinkley, P.S., Kelley, J.M.,
Klimek, K.M., Kelley, J.C., Liu, L.-I., Marmaros, S., Merrick, J.M.,
Moreno-Palauques, R.F., McDonald, L.A., Nguyen, D.T., Pellegrino, S.M.,
Phillips, C.A., Ryder, S.E., Scott, J.L., Saudek, D.M., Shirley, R.,
Shall, K.V., Springs, T.A., Utterback, T.R., Weidman, J.F., Li, Y.,
Bednarik, D.P., Cao, L., Cepeda, M.A., Coleman, T.A., Collins, E.-J.,
Dumke, D., Feng, P., Ferrie, A., Fischer, C., Hastings, G.A., He, W.-W.,
Hu, J.-S., Greene, J.M., Gruber, J., Hudson, P., Kim, A., Kozak, D.L.,
Kunsch, C., Ji, H., Li, H., Meissner, P.S., Olsen, H., Raymond, L., Wei,
Y.-F., Wing, J., Xu, C., Yu, G.-L., Ruben, S.M., Dillion, P.J., Fannon,
M.R., Rosen, C.A., Haseltine, W.A. Fields, C., Fraser, C.M., and
Venter, J.C.

TITLE

JOURNAL
MEDLINE
COMMENT

Initial Assessment of Human Gene Diversity and Expression Patterns
Based Upon 83 Million Basepairs of cDNA Sequence
Nature 377, 3-174 (1995)

Contact: Venter, JC

Contact: Venter, JC
 The Institute for Genomic Research
 932 Clopper Rd, Gaithersburg, MD 20878
 Tel: 3018699056
 Fax: 3018699423

Email: tddbinfo@tddb.tiar.org

For clone availability, additional sequence and expression

information related to

Des primer: M13 paterc
(labinfo@tab.tigr.org)

Location/Qualifiers

source

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/organism="Homo sapiens"  
/db_xref="ATCC (inhost):102309"  
/db_xref="taxon:9606"  
/clone_lib="Human Uterus"
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PRIGIN					

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Best Local Similarity:	04.5%	Score 361;	DB 14;	Length 413;

		Identity 94.5%;	Pred.No. 1e-41;	Mismatches	0;	Indels	1;	Gaps	1;
		Matches	381;	Conservative	0;				
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y	4107	CATGGTGTGGCATGGGCTGGGATCCTTCACCAATGTCAACTCCAGATGCTCTACTT	4166.						
b	61	CATGGTGTGGCATGGGCTGGGATCCTTCACCAATGTCAACTCCAGATGCTCTACTT	120						
y	4167	CGCCCTGATCTGGTTTTCAATGATACGCATGCACAAAGTCCCGGATGTACAGCCAGTG	4226						
b	121	CGCCCTGATCTGGTTTTCAATGATACGCATGCACAAAGTCCCGGATGTACAGCCAGTG	180						
y	4227	TGTCGGAATGAGGCACCTCTCTCAAGATTTGGATGGCTCCAAATACCCGCCGGAATT	4286						
b	181	TGTCGGAATGAGGCACCTCTCTCAAGATTTGGATGGCTCCAAATACCCGCCGGAATT	240						
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b	241	CTGTGCGATGAAGCAGCTGCTACTCTTCAGCATTTCCAGTGGATGGGCTGAAAAATCA	300						

[illegible]

BASE COUNT
percent

211 a	118 c	168 g	139 t	1 others
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[illegible]

RESULT 12
AA230070
LOCUS
DEFINITION
AA230070
ACCESSION
VERSION
AA230070.1
GI:1852363
349 bp mRNA linear EST 21-AUG-1997
nc49b08.s1 NCI-CPAP_Pr3 Homo sapiens cDNA clone IMAGE:1011443
similar to gb:M3263 ANDROGEN RECEPTOR (HUMAN);, mRNA sequence.

KEYWORDS EST.
SOURCE human.
ORGANISM Homo sapiens
REFERENCE Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
AUTHORS 1 (bases 1 to 349)
TITLE NCI-CGAP <http://www.ncbi.nlm.nih.gov/ncicgap>.
JOURNAL National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
Unpublished (1997)
CONTACT: Robert Strausberg, Ph.D.
JOURNAL Tumor Gene Index
CONTACT: cgapbs-email.nih.gov
COMMENT Email: [email.nih.gov](mailto:cgapbs-cgapbs-email.nih.gov
Tissue Procurement: W. Marston Linehan, M.D., Rodriyo Chuaqui, M.D.
; Michael Emmert-Buck, M.D., Ph.D.
cDNA Library Preparation: David B. Krizman, Ph.D.
cDNA Library Arrayed by: Genome Systems Inc., Greg Lennon, Ph.D.
DNA Sequencing by: Washington University Genome Sequencing Center
Clone distribution: NCI-CGAP clone distribution information can be
found through the I.M.A.G.E. Consortium/LIHL at:
www-bio.lnlni.gov/bbrp/image/image.html
Seq primer: -4lm13 fwd. ET from Amersham
High quality sequence stop: 230.

FEATURES
SOURCE

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1. .349
Location/Qualifiers
/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="IMAGE:1011443"
/clone_lib="NCI_CGAP_Pr3"
/sex="Male"
/dev_stage="45 years old"
/lab_host="DH10B"
/note="Vector: PAMP10; Site_1: NotI; Site_2: EcoRI; 1st
strand cDNA was primed with oligo(dT)17 on 50 ng of
DNase-treated, total cellular RNA obtained from 5,000-10
,000 microdissected cells histologically-determined to be
fully malignant prostate cancer cells. Double-stranded
cDNA was ligated to EcoRI adaptors, 5 cycles of PCR
applied to the cDNA with an adaptor-specific primer, and
the resulting PCR product subcloned into PAMP10 by the
UDG-cloning method (Life Technologies). Average insert
size is 600 bp. NOTE: Not directionally cloned. This
library was constructed by David Krizman."
64 a 105 c 57 g 123 t
BASE COUNT

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BASE COUNT      64 a 105 c 57 g 123 t
ORIGIN          library was constructed by David Krizman.

Query Match      6.8% Score 347.4; DB 9; Length 349;
Best Local Similarity 99.7% Pred. No. 9.2e-40;
Matches 348; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

OY 4540 GTGGACTTCCGGAAATGATGGCAGAGATCATCTCTGTGCAAGTGCCCAAGATCTTTCT 4599
Db 1 GTGGACTTTCGGAAATGATGGTAGAGATCATCTCTGTGCAAGTGCCCAAGATCTTTCT 60
OY 4600 GGGAAAGTCAAGCCCATCTATTTCCACACCCAGTGAAGCATTTGGAACCCCTATTTCCCCA 4659
Db 61 GGGAAAGTCAAGCCCATCTATTTCCACACCCAGTGAAGCATTTGGAACCCCTATTTCCCCA 120
OY 4660 CCCAGCTCATGCCCCCTTTCAGATGCTCTGCTGCCGTGTTAACTCTGTGCACTACTCTCT 4719
Db 121 CCCAGCTCATGCCCCCTTTCAGATGCTCTGCTGCCGTGTTAACTCTGTGCACTACTCTCT 180
OY 4720 GCAGTGCCCTGGGGAATTTCTCTATTGATGTACAGTCTGTCATGAACATGTTCTCGAAT 4779
Db 181 GCAGTGCCCTGGGGAATTTCTCTATTGATGTACAGTCTGTCATGAACATGTTCTCGAAT 240
OY 4780 TCTATTGTGCTGGGCTTTTTTTTCTCTCTCTCTCTCTCTTTCTTTTCTCTCTCCCTCAT 4839
Db 241 TCTATTGTGCTGGGCTTTTTTTTCTCTCTCTCTCTCTCTTTCTTTTCTCTCTCTCCCTCAT 300
OY 4840 CTAACCCCTCCCATGGCACCTTCAGACTTTGCTCCCATTTGGCTGGCTCCCTA 4988
Db 301 CTAACCCCTCCCATGGCACCTTCAGACTTTGCTCCCATTTGGCTGGCTCCCTA 349

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QY	4945	CAGTGTCAAGTTGCTGTTTACAGCAGCTACTCTGTGGCCAGCCACACAAACGTTTACTT	5004
Db	137	CAGTGTCAAGTTGCTGTTTACAGCAGCTACTCTGTGGCCAGCCACACAAACGTTTACTT	78
QY	5005	ATCTTATGCCACGGAAAGTTTAGAGAGCTAAGATTATCTGGGGAATCAAAACAAAAAC	5064
Db	77	ATCTTATGCCACGGAAAGTTTAGAGAGCTAAGATTATCTGGGGAATCAAAAC-ACAGAC	19
QY	5065	AAGCAAAACAAAAAAA	5082
Db	18	AAGCAAAACAAAAAAA	1
RESULT	14		
LOCUS	AI315085/c		
DEFINITION	u323g04.x1 Sugano mouse kidney mkia Mus musculus cDNA clone IMAGE:1920822 3' similar to gb:X53779 Mouse mRNA for androgen receptor (MOUSE);, mRNA sequence.		
ACCESSION	AI315085	536 bp	mRNA linear EST 17-DEC-1998
VERSION	AI315085.1	GI:4030352	
KEYWORDS	EST.		
SOURCE	house mouse.		
ORGANISM	Mus musculus		
REFERENCE	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.		
AUTHORS	1 (bases 1 to 536) Marra,M., Hillier,L., Allen,M., Bowles,M., Dietrich,N., Dubuque,T., Geisel,S., Kucaba,T., Lacy,M., Le,M., Martin,J., Morris,M., Schellenberg,K., Steptoe,M., Tan,F., Underwood,K., Moore,B., Theising,B., Wyllie,T., Lennon,G., Soares,B., Willson,R. and Waterston,R.		
TITLE	The WashU-HMI Mouse EST Project		
JOURNAL	Unpublished (1996)		
COMMENT	Contact: Marra M/Mouse EST Project WashU-HMI Mouse EST Project Washington University School of MedicineP 4444 Forest Park Parkway, Box 8501, St. Louis, MO-63108 Tel: 314 286 1800 Fax: 314 286 1810 Email: mouseest@watson.wustl.edu This clone is available royalty-free through LNL ; contact the IMAGE Consortium (info@image.llnl.gov) for further information. MGI:977114		
FEATURES	Seq primer: custom primer used High quality sequence stop: 487.		
source	Location/Qualifiers 1..536 /organism="Mus musculus" /strain="C57BL" /db_xref="taxon:10090" /clone="IMAGE:1920822" /clone_lib="Sugano mouse kidney mkia" /sex="female" /dev_stage="adult" /lab_host="DH10B" /note="Organ: kidney; Vector: pME18S-FL3; Site.1: DraIII (CACTGTGTG); Site.2: DraIII (CACTGTGTG); 1st strand CDNA was primed with an oligo(dT) primer [ATGTGGCGCTTTTCTTTTCTTTT]; double-stranded cDNA was ligated to a DraIII adaptor [TCTTGGCTCACTGG], digested and cloned into distinct DraIII sites of the pME18S-FL3 vector (5' site CACTGTGTG, 3' site CACTGTGTG). XhoI should be used to isolate the cDNA insert. Size selection was performed to exclude fragments <1.5kb. Library constructed by Dr. Sumio Sugano (University of Tokyo Institute of Medical Science). Custom primers for sequencing: 5' end primer CTTCGTGCTCTAAAGCTGG and 3' end primer CGACCTGCAGCTCGAGCACA."		
BASE COUNT	181 a	101 c	129 g 124 t
ORIGIN	1 others		
Query Match	6.3%; Score 319; DB 9; Length 536;		

